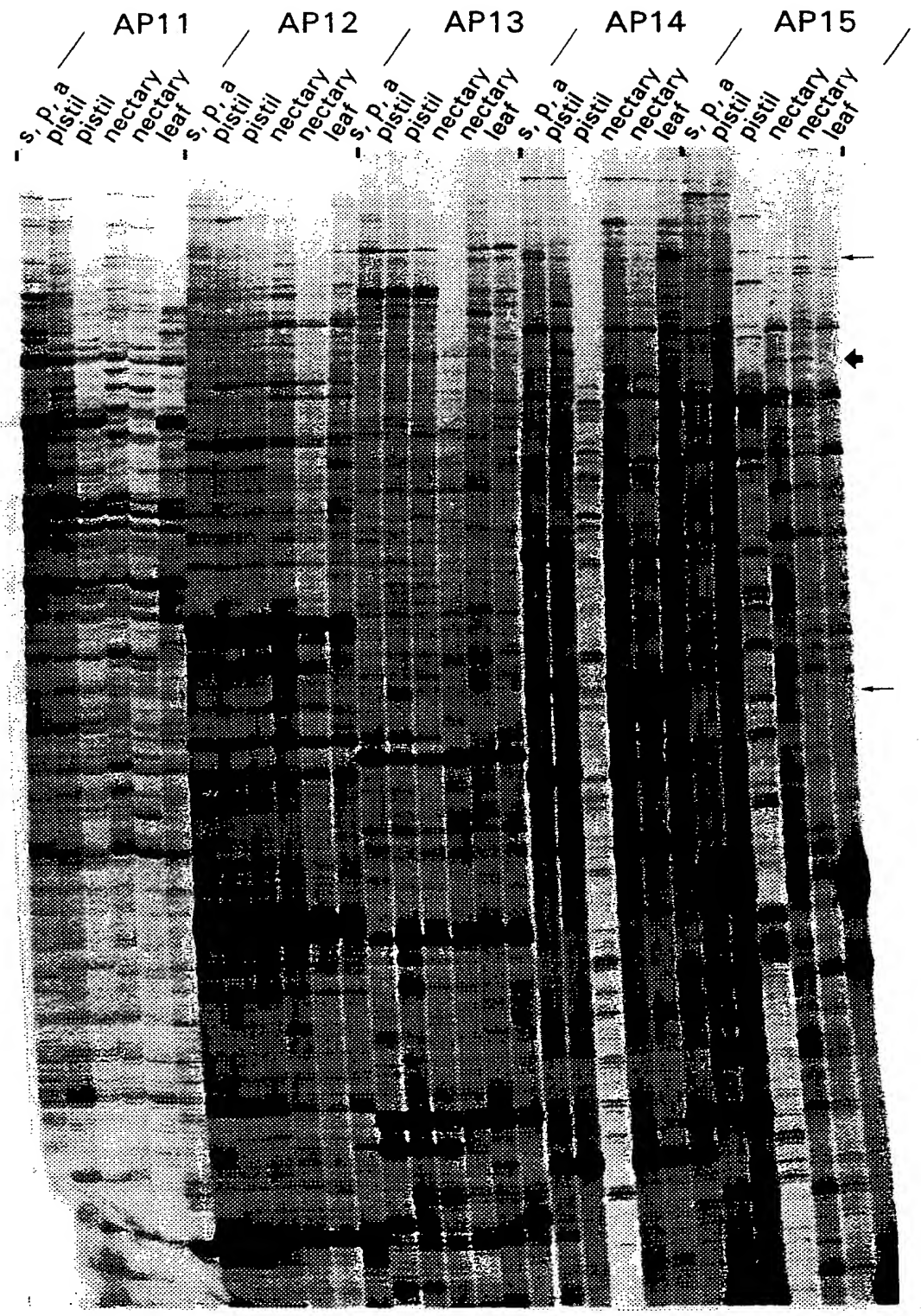

AP11
AP12
AP13
AP14
AP15
s, p, a
pistil
pistil
nectary
nectary
leaf

FIG.1

```
1     TGATCCTGTT CGAGAAGCTA CAAAATCAAA AGAAGGTGTA GAAATCATTA
51    TCAACATTGA AGATGATAAT TCTGATAACG CATTGCAGTC CATGGAGAAG  prat 119 ←
101   GATTTTTCCA GACTGCGGAC ATCAAAATAA GCAAGAAGAT GATCAAAAAA
151   TGACAAAGCT AAGGAGTTTG AAGTAAGGCA AGGAACTTGA CACTGAATAT
201   CTAAGCTAAT TAGCAAGACT TTAGCAGCTT GTAATATTTA GTGTTTGTGA
251   GGTGTTACCT TATAATTAGC TTGTAGCATA GCCTTCCCAC TAATAATTCT  prat 122 ←
301   GCTTAGCGAA TCTTATATAT GGGAAATACT TACACTAGTA TGCATCTTCT
351   ATATACATGT TTGGCACTTG ACTATACATA GAAAAATTAA CAAGCATTTC
401   TCACCTCAAT TTGTCACTTA CTTATAAGTA GCTGAATAAT ATAATGCAAT
451   TTTCACCCC
```

FIG.2

```
1     TCGAGCGGCC GCCCGGGCAG GTATTCAACA AGAGTATTCA CCACTTGAAC
51    TCAAAAGGGG CTTCACTAAA AAAAAATCAT GGCGCAATTA CGTGCTGATG prat 129 ⟶
101   ACTTGTCTTT CATATTTGGC CTTCTTGGTA ATATTGTATC ATTCATGGTC
151   TTCCTAGCAC CCGTGCCAAC ATTTTACAAA ATATATAAAA GGAAATCATC
201   AGAAGGATAT CAAGCAATAC CATATATGGT AGCACTGTTC AGCGCCGGAC
251   TATTGCTATA TTATGCTTAT CTCAGGAAGA ATGCCTATCT TATCGTCAGC
301   ATTAATGGCT TTGGATGTGC CATTGAATTA ACATATATCT CTCTGTTTCT
351   CTTTTACGCG CCCAGAAAGT CTAAGATTTT CACAGGGTGG CTGATGCTCT
401   TAGAATTGGG AGCCCTAGGA ATGGTGATGC CAATTACTTA TTTATTAGCA
451   GAAGGCTCAC ATAGAGTGAT GATAGTGGGA TGGATTTGTG CAGCTATCAA
501   TGTTGCTGTC TTTGCTGCTC CTTTAAGCAT CATGAGGCAA GTAATAAAAA
551   CAAAGAGTGT AGAGTTCATG CCCTTCACTT TATCTTTGTT CCTCACTCTC
601   TGTGCCACTA TGTGGTTTTT CTATGGGTTT TTCAAGAAGG ACTTTTACAT
651   TGCGTTTCCA AATATACTGG GCTTTCTATT CGGAATCGTT CAAATGCTAT
701   TATATTTTGT TTACAAGGAT TCAAAGAGAA TAGATGATGA AAAATCTGAT
751   CCTGTTCGAG AAGCTACAAA ATCAAAAGAA GGTGTAGAAA TCATTATCAA
801   CATTGAAGAT GATAATTCTG ATAACGCATT GCAGTCCATG GAGAAGG
```

FIG.3

```
1     TCGAGCGGCC GCCCGGGCAG GTATTCAACA AGAGTATTCA CCACTTGAAC
51    TCAAAAGGGG CTTCACTAAA AAAAAATCAT GGCGCAATTA CGTGCTGATG
101   ACTTGTCTTT CATATTTGGC CTTCTTGGTA ATATTGTATC ATTCATGGTC
151   TTCCTAGCAC CCGTGCCAAC ATTTTACAAA ATATATAAAA GGAAATCATC
201   AGAAGGATAT CAAGCAATAC CATATATGGT AGCACTGTTC AGCGCCGGAC
251   TATTGCTATA TTATGCTTAT CTCAGGAAGA ATGCCTATCT TATCGTCAGC
301   ATTAATGGCT TTGGATGTGC CATTGAATTA ACATATATCT CTCTGTTTCT
351   CTTTTACGCG CCCAGAAAGT CTAAGATTTT CACAGGGTGG CTGATGCTCT
401   TAGAATTGGG AGCCCTAGGA ATGGTGATGC CAATTACTTA TTTATTAGCA
451   GAAGGCTCAC ATAGAGTGAT GATAGTGGGA TGGATTTGTG CAGCTATCAA
501   TGTTGCTGTC TTTGCTGCTC CTTTAAGCAT CATGAGGCAA GTAATAAAAA
551   CAAAGAGTGT AGAGTTCATG CCCTTCACTT TATCTTTGTT CCTCACTCTC
601   TGTGCCACTA TGTGGTTTTT CTATGGGTTT TTCAAGAAGG ACTTTTACAT
651   TGCGTTTCCA AATATACTGG GCTTTCTATT CGGAATCGTT CAAATGCTAT
701   TATATTTTGT TTACAAGGAT TCAAAGAGAA TAGATGATGA AAAATCTGAT
751   CCTGTTCGAG AAGCTACAAA ATCAAAAGAA GGTGTAGAAA TCATTATCAA
801   CATTGAAGAT GATAATTCTG ATAACGCATT GCAGTCCATG GAGAAGGATT
851   TTTCCAGACT GCGGACATCA AAATAAGCAA GAAGATGATC AAAAAATGAC
901   AAAGCTAAGG AGTTTGAAGT AAGGCAAGGA ACTTGACACT GAATATCTAA
951   GCTAATTAGC AAGACTTTAG CAGCTTGTAA TATTTAGTGT TTGTGAGGTG
1001  TTACCTTATA ATTAGCTTGT AGCATAGCCT TCCCACTAAT AATTCTGCTT
1051  AGCGAATCTT ATATATGGGA AATACTTACA CTAGTATGCA TCTTCTATAT
1101  ACATGTTTGG CACTTGACTA TACATAGAAA AATTAACAAG CATTTCTCAC
1151  CTCAATTTGT CACTTACTTA TAAGTAGCTG AATAATATAA TGCAATTTTC
1201  ACCCC
```

FIG. 4

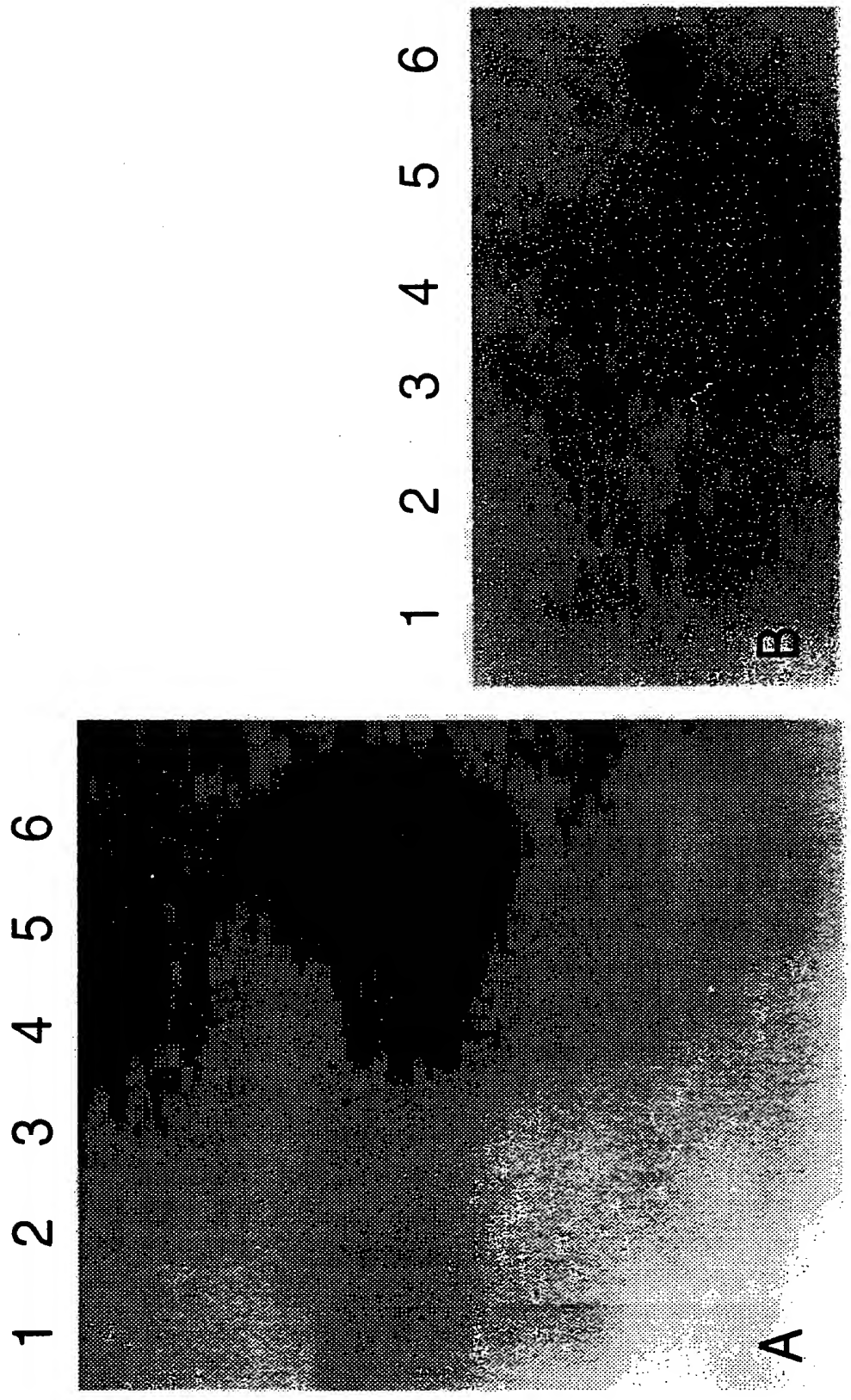


FIG.5

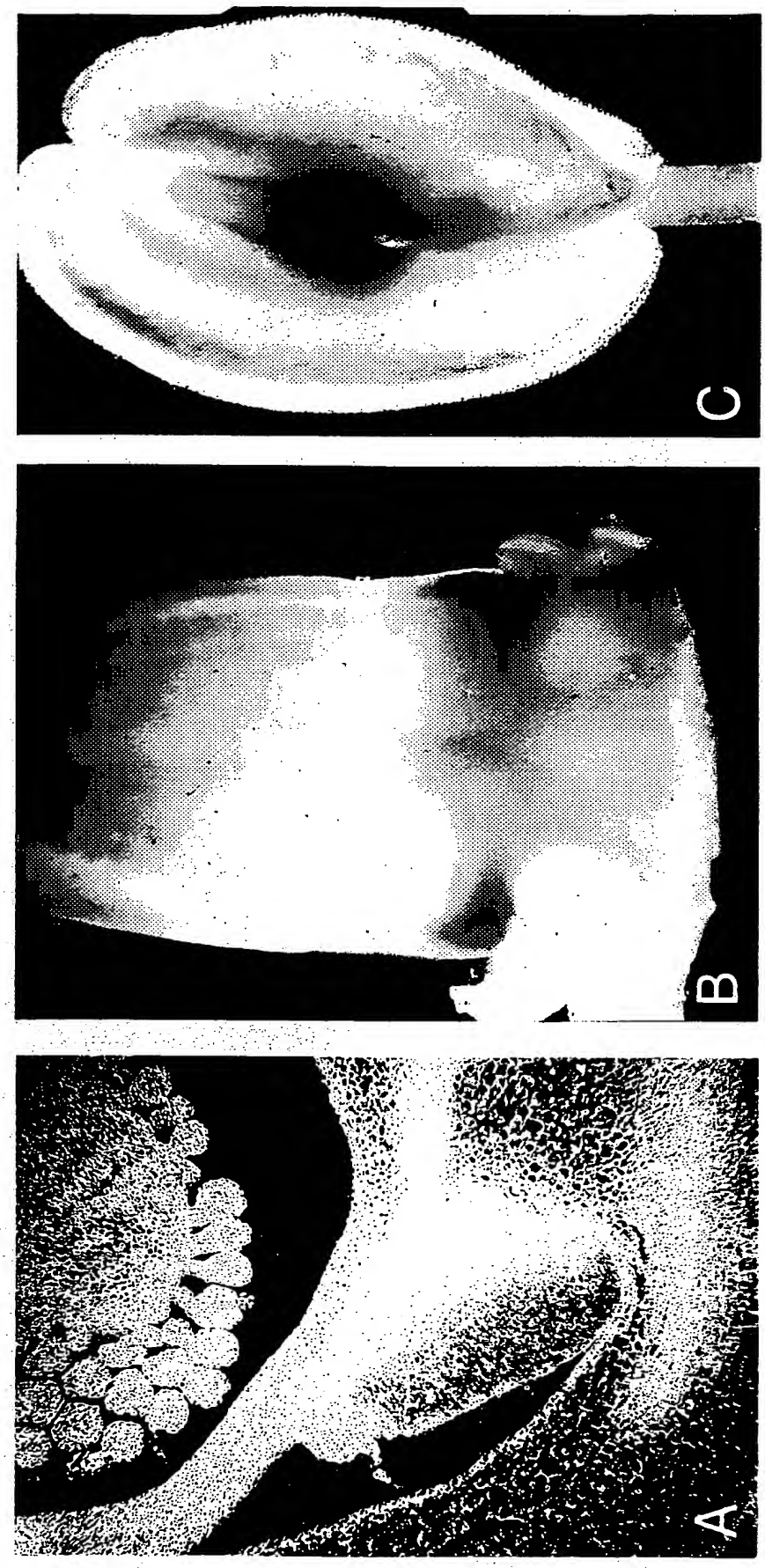


FIG.6

```
1     CCTAGGAGAAATCAAGCCTACTCTTAAGATGGATGACTCACTTGCCCCGA
51    TGGTAAGGTGAAGGATCTGTTGATTAGAGTTGGGAAGTTCATGTTCTCTG
101   CTGATTTTATTATTCTAGACTATGAAGAGGACCAAGAAGCTCCAATAATT
151   TTGGGAAGAGCATTCTTAATCACATCGATGGCAATTATTGACATGGAACT
201   TGGGGAGATGACTGTGAGAGCGCATGGAGAAAAGGTTACTTTCAAGGTTT
251   ATAATAAAAAGGATCATATGGCTAAGTTTGAAGAGTGTTCTTTGATAGAA
301   TGTGTCAGACGAGAACATGAAAGTAAACCGAAAGAGGTGTTTGAGCGGAA
351   TGTAGAACAAAGTGACCACGGCACAATAATTGACAAGTTGAAGGAAAATT
401   CACCTAAAGGAAGGAAGAAGACAAAAGTTCGTCGTAACAAGAGGAGACGT
451   AAATGCTGGAAGTGAGCTTAAAGGTGTTGTCGTACTACGACGTTAACTAA
501   GGCGCTTGTCGGGAGGCAACCCTAGCTTTGTATGTAAATGTAAAAGTAAA
551   AAATATATATATAGAAAAAGGAAAATACAAAAAGAGTCGTGCCGCGACGT
601   TAAATCAAGCGCTTGTTGGAAGGCAACCCAATTTTTATTGTTTTAGTTGT
651   TTTACTTATTTAGTATTACGTAGTTTCTTGTTGTTTTTGTAGGGCTCGGG
701   ACTTTCGGAAGGTGAGGTAATTTCAAGGCATCGCGGTGTGTATTGCAGCG
751   AGGTAAGTGTAAGAGTTGAGTTGGAAGCGTTTGGCCAAGTGTTGCACCGT
801   GAGAGGCTTTCAACCTGTTGCGACACGTGAAAAATTAAGAGCCAGATCTG
851   CTACATTAGCACTGAAGCATCGCTTGGCCAATAGCTTGGAATGGAAGCAA
901   GAATTCAAACCAAAATCAGAAACGCCACAAGAGATGTGTCGCACACTGCA
951   AAGCTTTGTGCAAACTAGTGAACGCAGAAATAGAAATGCTACAGCCCATG
1001  CGTCGCTTGGCTTATGGCAGGCAGCAAAAATTCAGCAGCAAAACAGAAAC
1051  GCTGCGAGAAACGCGTCGCATACGCCATAGCTTTGTGTCAAACAGAACGT
1101  CCAGAAATTGAAAAGCTATAAGCCTGCGTCGCTTGGCTCATGGCGTGCAG
1151  ACTAGAAAAGCTCTAGCAGATGCGTCGCGTATTGTATAGCTTGGTGTGAA
1201  ACAGAAAGTTCGAAACTTGGAAAACGATAACCCAGCGTCGCCTCTTCAAC
1251  CGCGTCCAGGTAAGTTCAAGATTCTTACGGGTTGACCCATTAACCCATTG
1301  ATCGGCTGATTATAAACAATAAAACATCACCTTCAACTATCACATGATTT
1351  CATAAGTTTGACCTAGGATATTTTATATATATATATATATATATACACAC
```

FIG.7

```
1401  ACACACCATTTCCAGCGATCTTACCTCATTTTTATTCAAACCATTTTTCT
1451  GCTTCAAAAGTTTAAATTATTAATATGATAAGTCATCCATAGTCAAACAA
1501  GATTTTCTATACTATTTTGTCCCTTGTAATTTTAAAAAAAAAATGAGCGA
1551  TGGTAAGATAAACATTGTTTGCAAGTGTACAATTTTAGTATATGCAAACC
1601  AACGCTTCTTCTTCCAACTATCACCTAAAACTACATCATTTATGGCGGGC
1651  GGACTAGACGTAGCCAAATATAAAAACGCAATGGCCATTCAGTTCATGTC
1701  ATTTTTATATCCTTCATCCAATAATATTACTCAAAATTGATGTACAGTTT
1751  GGTCTCTGATGTGCACTTTACTATACGTAATACGGAATTTACATTATAAT
1801  TAAAGAGAACTGTTCCACTAAATTTTAATGATTTAATTAATTTAACTCGG
1851  TTACTTGTATTATTATTATTGCTGTATTTGTTTGTCATTTGAATTTGGCA
1901  CCGCAGATTTTTGTATGCAATTAACCCTCATATATCTTTTGGCCAAATAA
1951  AGAAAAAGTCTGCATATTTCTTGCCAAACATTTATCATACTTTACCGAAT
2001  TCTTGTTTTTTGTTTCTCTGTTGTTGTTCTCCACTATAAATAACATTTGC
2051  AGTGAGTAAAGTTTCTTCAGGTCTCTTTTGTAGATTCAACAAGAGTATTC
2101  AGCACTTGAACTCAAAAGGGGCTTCACTAAAAAAAATCATG
```

FIG.7(CONTIN.)

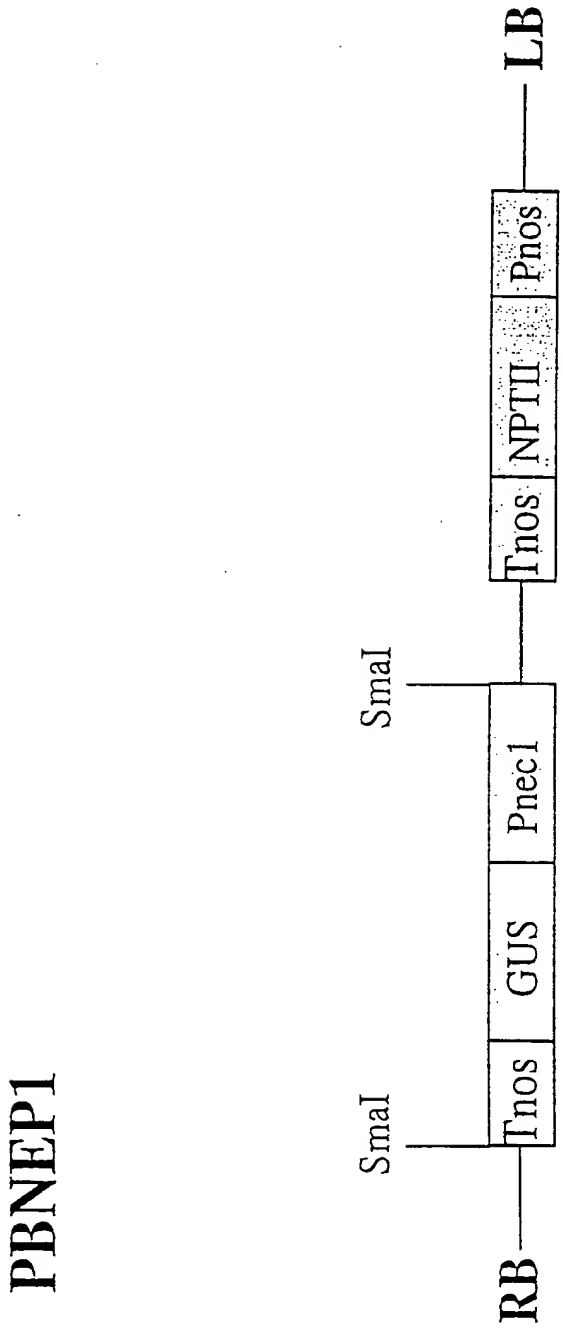


FIG. 8

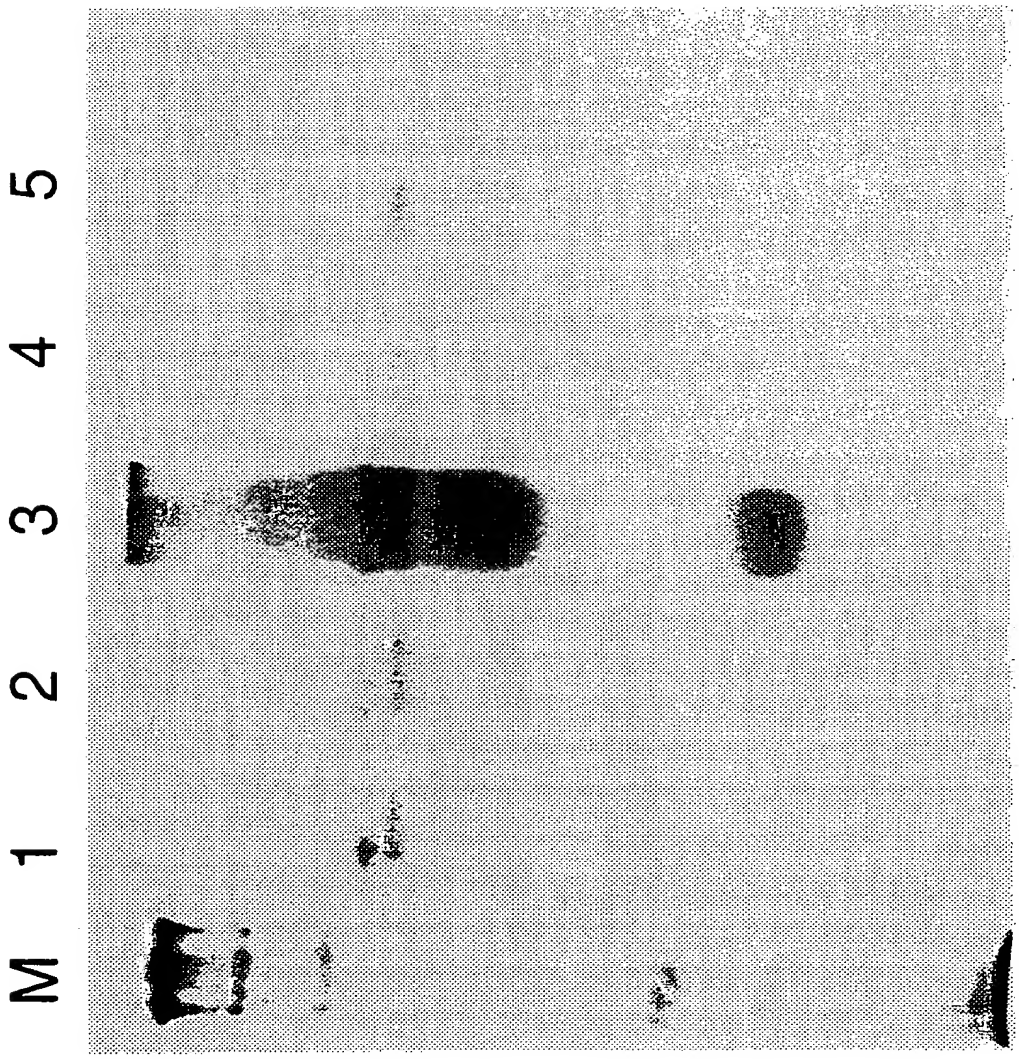


FIG. 9

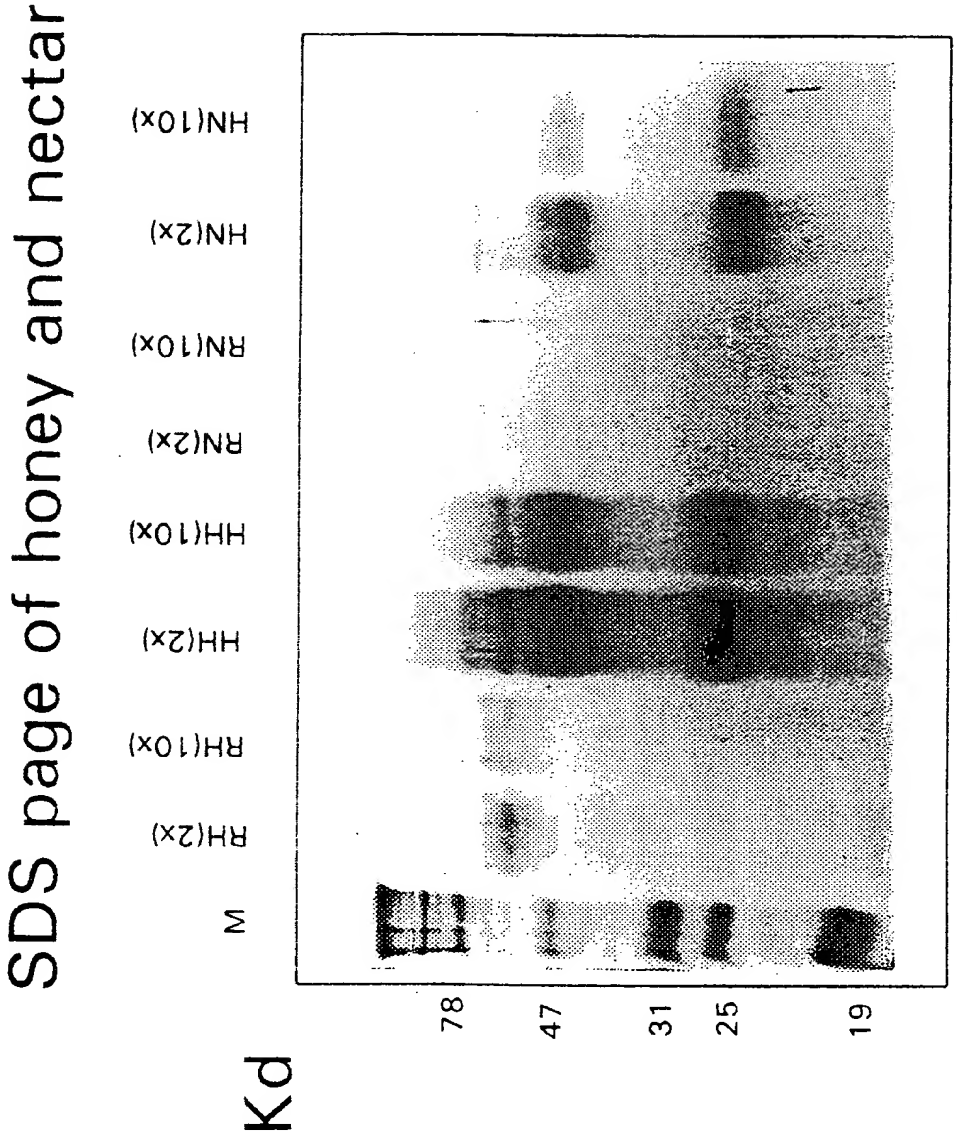
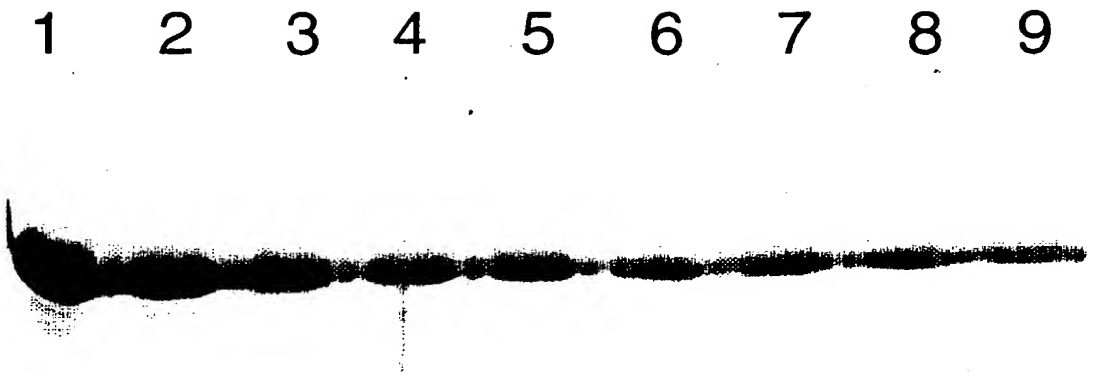
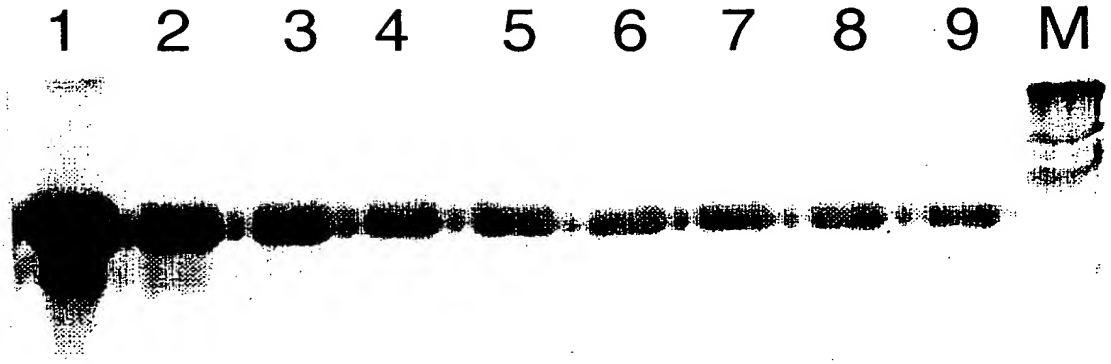

SDS page of honey and nectar
M
RH(2x)
RH(10x)
HH(2x)
HH(10x)
RN(2x)
RN(10x)
HN(2x)
HN(10x)
Kd
78
47
31
25
19

FIG.10



A



B

FIG. 11

```
===17-APR-1998=============================================================PC/GENE===

****************************************
* ALIGNMENT OF TWO PROTEIN SEQUENCES. *
****************************************

The two sequences to be aligned are:

PCVH29.
Total number of residues: 60.

GER1.
Total number of residues: 211.

Comparison matrix  : Structure-genetic matrix.
Open gap cost      : 7
Unit gap cost      : 1

The character to show that two aligned residues are identical is '|'

PCVH29     - MKMFLPILFTISLLFSSSHASVLDFCVADPSLPDGPAGYSCKEPAKVTVD -50
             |||    | |  ||  | | ||| |||||||  |  | |||||  |  ||
GER1       - MKMRIQIFFILSLFSSISFASVQDFCVADPKGPQNPSGYSCKNPDQVTEN -50

PCVH29     - DFVFHGLGTA                                         -60
             || |  ||| |
GER1       - DFAFSGLGKAGNTSNVIKAAVTPAFAPAFAGLNGLDVSLARLDLAGGGVI -100

GER1       - PLHTHPGASEVLVVIQGTICAGFISSANKVYLKTLSRGDSMVFPQGLLHF -150

GER1       - QLNSGKGPALAFVAFGSSSPGLQILPFALFANDLPSELVEATTFLSDEEV -200

GER1       - KKLKGVLGGTN -211


Identity  : 36 ( 60%)
Number of gaps inserted in PCVH29: 0
Number of gaps inserted in GER1: 0

===17-APR-1998=============================================================PC/GENE===
```

FIG. 12

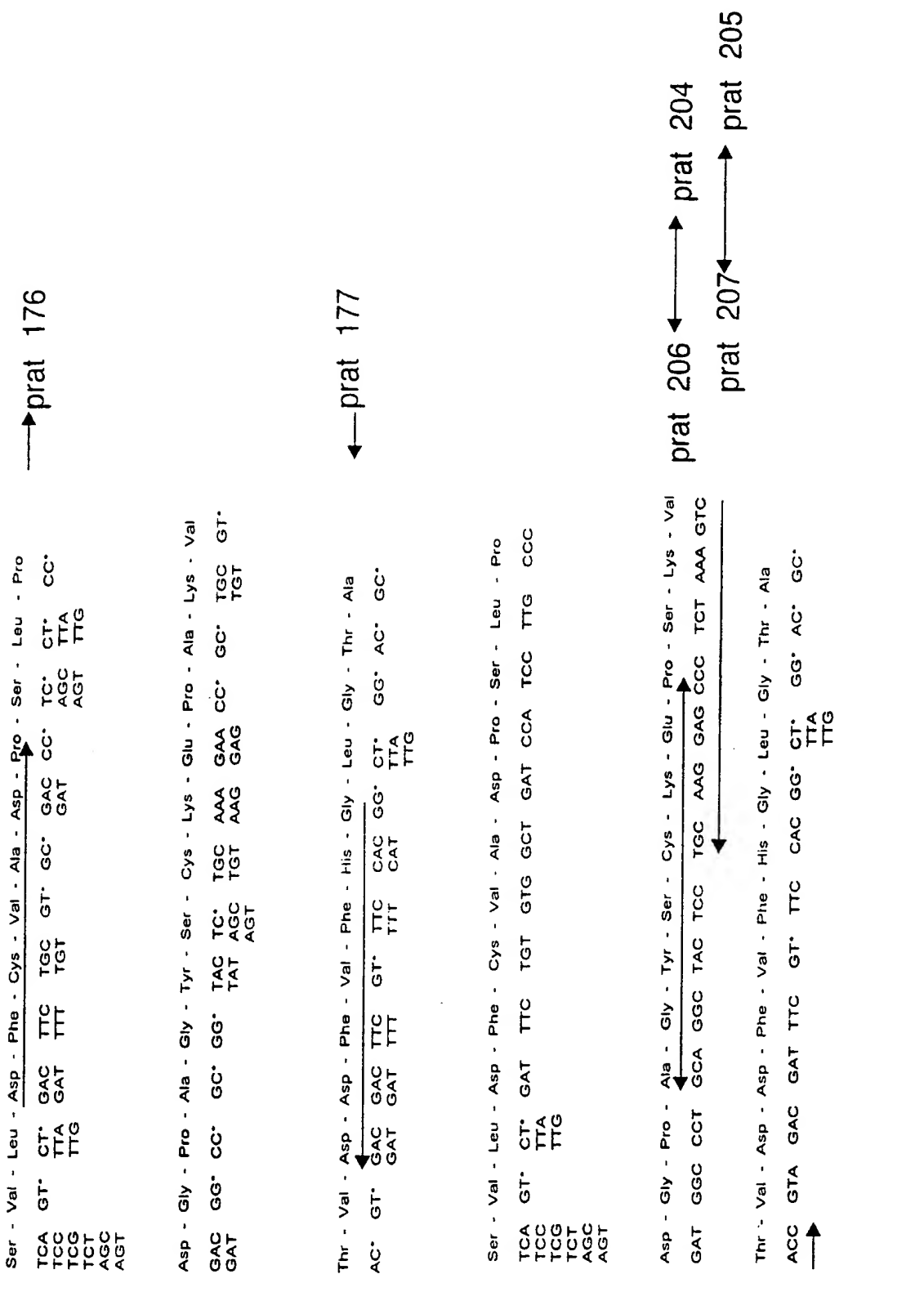


FIG.13

```
MAR5H6  CGCCCGGGCTGGTAAACAAAGTACGTGTATACTCATTGTATTTCCTTAAA  50
MAR5R8  CGCCCGGGCTGGTAAACAAAGTACGTGTATACTCATTGTATTTCCTTAAA  50
MAR5R6  GGCCCGGGCTGGTAAACAAAGTACGTGTATACTCATTGTATTTCCTTAAA  50
MAR5H8  CGCCCGGGCTGGTAAACAAAGTACGTGTATACTCATTGTATTTCCTTAAA  50
        ************************************************

MAR5H6  AAAGCAACTGTCAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC  100
MAR5R8  AAAGCAACTGTCAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC  100
MAR5R6  AAAGCAACTGTCAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC  100
MAR5H8  AA-GCAACTGTCAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC   99
        ** ************************************************

MAR5H6  CCCTATTGGACAACACGAACTCTAAGAGGGCAATCAGACACACCAGCCAT  150
MAR5R8  CCCTATTGGACAACACGAACTCTAAGAGGGCAATCAGACACACCAGCCAT  150
MAR5R6  CCCTATTGGACAACACGAACTCTAAGAGGGCAATCAGACACACCAGCCAT  150
MAR5H8  CCCTATTAAACACCACGAACTCTAAGAGGGCAATCAGACACACCAGCCAT  149
        *******..*** ************************************

MAR5H6  TGCACTTGTGAAGATGTTTCTTCCAATTCTCTTCACCATTTCCCTCCTCT  200
MAR5R8  TGCACTTGTGAAGATGTTTCTTCCAATTCTCTTCACCATTTCCCTCCTCT  200
MAR5R6  TGCACTTGTGAAGATGTTTCTTCCAATTCTCTTCACCATTTCCCTCCTCT  200
MAR5H8  TGCACTTATGAAGATGTTTCTTCCAATTCTCTTCACCATTTCCCTCCTCT  199
        ********.*************************************** 
        signal sequence ◄——► mature protein

MAR5H6  TCTCCTCCTCCCATGCTTCAGTGTTGGACTTCTGCGTAGCAGACCCATCC  250
MAR5R8  TCTCCTCCTCCCATGCTTCAGTGTTGGACTTCTGCGTAGCAGACCCATCC  250
MAR5R6  TCTCCTCCTCCCATGCTTCAGTGTTGGACTTCTGCGTAGCAGACCCATCC  250
MAR5H8  TCTCCTCCTCCCATGCTTCAGTGTTGGACTTCTGCGTAGCAGGCCCACCC  249
        ************************************.**** **
```

FIG. 14

tatgttccttccaattcttttcactatttctcttcttttctcttcttctcatgcttctgttcttgatttcg
acaaggaaggttaagaaaaagtgataaagagaagaaaaagagaagaagagtacgaagacaagaactaaagcctag

FIG.15

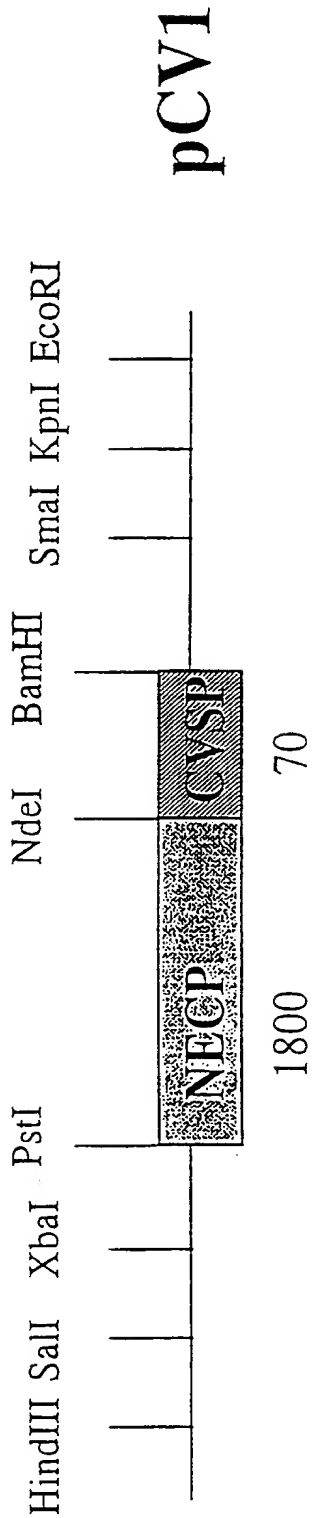

pCV1
HindIII SalI XbaI PstI
NdeI BamHI
SmaI KpnI EcoRI
NEGP
CVSP
1800
70

FIG.16

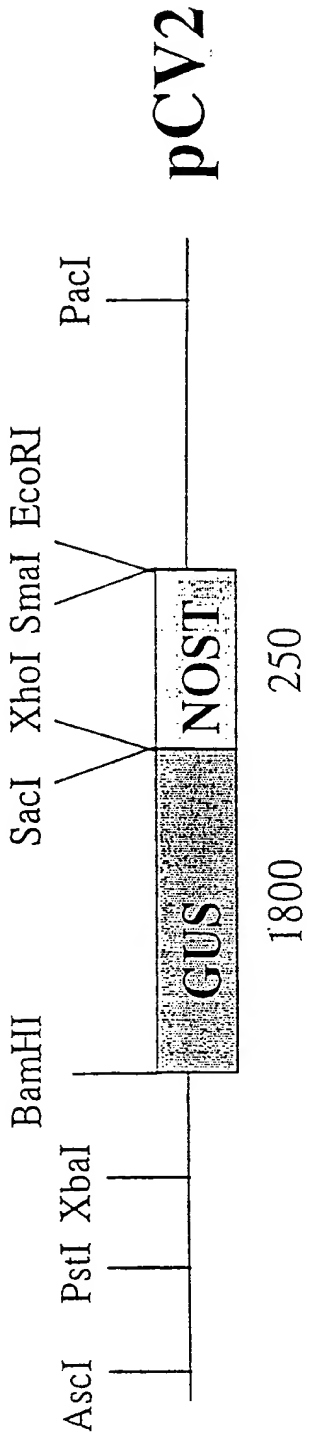

pCV2
PacI
EcoRI
SmaI
XhoI
SacI
NOST
250
GUS
1800
BamHI
XbaI
PstI
AscI

FIG.17

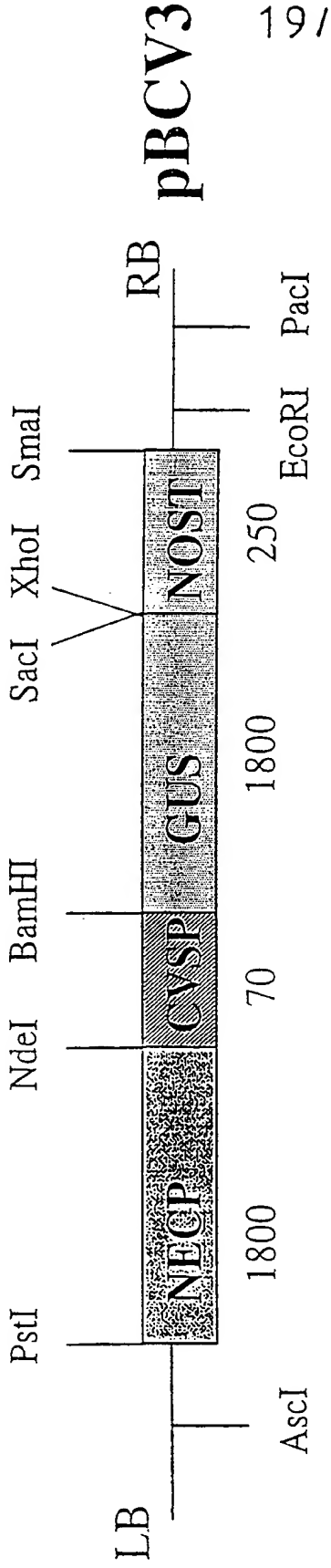

pBCV3
RB
PacI
EcoRI
SmaI
XhoI
SacI
NOST
250
GUS
1800
BamHI
CVSP
70
NdeI
NEGP
1800
PstI
AscI
LB

FIG. 18

```
1     TCTGAATACAAGCTGTGTGTGTAGAGAGATTTCATAAAGACAGCAAACAT
51    CCCTTCTTTTTGTTCTGTTTTAAAAGTTCCCTTCTTCAACCAGCTCTTTT
101   CCTCATCAGGGTAAGTTGCAAATAAAGGGGATGTTCCAGAATCAAGAAGA
151   GAAGATGTCAGACTCGCCTCAGAGGAAGATGGGAAGAGGAAAGATTGAGA
201   TTAAGAGGATTGAAAATACAACAAATCGTCAAGTCACTTTCTGTAAGAGA
251   AGAAATGGGTTGCTTAAAAAAGCTTATGAACTTTCTGTTCTTTGTGATGC
301   TGAAGTTGCTCTCATCGTTTTCTCAAGCCGTGGCCGCCTCTATGAATATG
351   CTAACAACAGTGTGAAGGCAACAATTGATAGATATAAGAAAGCATCCTCA
401   GATTCCTCCAACACTGGATCTACTTCTGAAGCTAACACTCAGTTTTATCA
451   ACAAGAAGCTGCCAAACTCCGAGTTCAGATTGGTAACTTACAGAACTCAA
501   ACAGGAACATGCTAGGCGAGTCTCTAAGTTCTCTGACTGCAAAAGATCTG
551   AAAGGCCTGGAGACCAAACTTGAGAAAGGAATTAGTAGAATTAGGTCCAA
601   AAAGAATGAACTCCTGTTTGCTGAGATTGAGTATATGCGAAAAAGGGAAA
651   TTGATTTGCACAACAACAATCAGATGCTTCGGGCAAAGATAGCTGAGAGT
701   GAAAGAAATGTGAACATGATGGGAGGAGAATTTGAGCTGATGCAATCTCA
751   TCCGTACGATCCAAGAGACTTCTTCCAAGTGAACGGCTTACAGCATAATC
801   ATCAATATCCACGCCAAGACAACATGGCTCTTCAATTAGTATAAGTTTAT
851   AATAAAATGCATGGTTTGAAGCACTCTGATTGTGGTGGATTTGGATTATG
901   TATAAGGGAGTGCAGGCCATTTGCCAATTATTGAAAGGTACTCAAACAGG
951   AAGTTGAAGAAGTTCATCATCTCTCTCATCTATATGTCTTAACAAAAGTC
1001  TTAGCTTATGGACTCTAAAACAAAGACTTAATTTAACATATAAATATAAT
1051  TGTGTAATGCTGTTGTATTGTATGGTATGTATCCAAAAACATTAATAACC
1101  TATCTTTTTCTTCAAATTATGTCTCCTTTGATACAAACTACTAACATATT
1151  TTCTTAT
```

MADS-box

K-box

FIG.19